

SEQUENCE LISTING

5 <110> Larsen, Christian P.
 Pearson, Thomas C.
 Waller, Edmund K.
 Adams, Andrew B.

10 <120> METHODS OF INDUCING ORGAN TRANSPLANT TOLERANCE AND
 CORRECTING HEMOGLOBINOPATHIES

15 <130> D0136NP/30436.58USU1

20 <140> Not yet known
 <141> 2002-01-25

25 <150> 60/264,528
 <151> 2001-01-26

30 <150> 60/303,142
 <151> 2001-07-05

35 <160> 20

40 <170> PatentIn Ver. 2.1

45 <210> 1
 <211> 1152
 <212> DNA
 <213> Artificial Sequence

50 <220>
 <223> Description of Artificial Sequence: L104E1g
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 agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggtaactggc cagcagccga 120
 ggcatcgcta gctttgtgtg tgtagtatgca tctccaggca aagccactga ggtccgggtg 180
 acagtgcctc ggcaggctga cagccaggtg actgaagtct gtgcggcaac ctacatgatg 240
 gggaatgagt tgacacctt agatgattcc atctgcacgg gcacccctcag tggaaatcaa 300
 gtgaacctca ctatccaagg actgaggggcc atggacacacgg gactctacat ctgcaagggtg 360
 gagctcatgt acccaccgccc atactacgag ggcataaggca acggaaccca gattttatgta 420
 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaaactcac 480
 acatccccac cgtcccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540
 ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtgggtgtg 600
 gacgtgagcc acgaagaccc tgaggtcaag ttcaacttgtt acgtggacgg cgtggagggtg 660
 cataatgccca agacaaagcc gcgggaggag cagataacaaca gcacgtaccg tgggtcagc 720
 gtcctcaccc tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780
 aacaaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
 gaaccacagg tgtacaccct gccccatcc cgggatgagc tgacccaagaa ccaggtcagc 900
 ctgacctgccc tggtaaaagg cttctatccc aegcagacatcg ccgtggagtg ggagagcaat 960
 gggcagccgg agaacaacta caagaccacg cctccctgtgc tggactccga cgcttccttc 1020
 ttcccttaca gcaagctcac cgtggacaag agcagggaa cgtcttctca 1080
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 ccgggttaat ga 1152

<210> 2
<211> 383
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: L104EIg
sequence

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1 5 10 15
Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
15 20 25 30
Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
35 40 45
20 Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
50 55 60
Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65 70 75 80
25 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
85 90 95
30 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100 105 110
Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
115 120 125
35 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140
Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
145 150 155 160
40 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
165 170 175
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
45 180 185 190
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
195 200 205
50 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
210 215 220
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
225 230 235 240
55 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
245 250 255

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
 260 265 270

5 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 275 280 285

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 290 295 300

10 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 305 310 315 320

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 15 325 330 335

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
 340 345 350

20 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 355 360 365

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 370 375 380

25 <210> 3
 <211> 1152
 <212> DNA
 30 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: L104EA29YIg
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 ggcacatcgcta gctttgtgt tgtagtatgca tctccaggca aataatactga ggtccgggtg 180
 40 acagtgcctc ggcaggctga cagccaggtg actgaagtct gtgcggcaac ctacatgatg 240
 gggaaatgagt tgacacctt agatgattcc atctgcacgg gcaccccttccag tggaaatcaa 300
 gtgaacctca ctatccaagg actgaggggcc atggacacacgg gactctacat ctgcaagggtg 360
 gagctcatgt acccaccgccc atactacgag ggcataaggca acggaaccca gattttatgtta 420
 45 attgatccag aaccgtgcccc agattctgtat caggagccca aatcttctga caaaaactcac 480
 acatccccac cgtcccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540
 cccaaaaccca aggacacccct catgatctcc cggacccctg aggtcacatg cgtgggtggtg 600
 gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 660
 cataatgccca agacaaagcc gcggggaggag cagtacaaca gcacgtaccc tggtggtcagc 720
 gtcctcacccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780
 50 aacaaaagccc tcccagcccc catcgagaaaa accatctcca aagccaaagg gcagccccga 840
 gaaccacagg tgtacacccct gccccccatcc cgggatgago tgaccaagaa ccaggtcagc 900
 ctgacctgcc tggtaaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
 gggcagccgg agaacaacta caagaccacg cctccctgtgc tggactccga cgctcccttc 1020
 ttcccttaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1080
 55 tgctccgtga tgcatacgaggc tctgcacaaac cactacacgc agaagagcct ctccctgtct 1140
 ccgggttaat ga 1152

<210> 4
<211> 383
<212> PRT
5 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: L104EA29YIg
sequence

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Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
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15 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
20 25 30

Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
35 40 45

20 Tyr Ala Ser Pro Gly Lys Tyr Thr Glu Val Arg Val Thr Val Leu Arg
50 55 60

Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
25 65 70 75 80

Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
85 90 95

30 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100 105 110

Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
115 120 125

35 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140

40 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
145 150 155 160

Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
165 170 175

45 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
180 185 190

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
195 200 205

50 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
210 215 220

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
55 225 230 235 240

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys

	245	250	255
	Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile		
	260	265	270
5	Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro		
	275	280	285
	Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu		
10	290	295	300
	Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn		
	305	310	315
15	Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser		
	325	330	335
	Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg		
	340	345	350
20	Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu		
	355	360	365
	His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		
25	370	375	380
	<210> 5		
	<211> 1152		
30	<212> DNA		
	<213> Artificial Sequence		
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35	<223> Description of Artificial Sequence: L104EA29LIG		
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	agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggtaactggc cagcagccga 120		
40	ggcatcgcta gctttgtgt tgagtatgca tctccaggca aattgactga ggtccgggtg 180		
	acagtgcctc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240		
	gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacaccttccag tggaaatcaa 300		
	gtgaacctca ctatccaagg actgagggcc atggacacacgg gactctacat ctgcaagggtg 360		
	gagctcatgt acccaccgccc atactacgag ggcataaggca acggaaccca gatttatgta 420		
45	attgatccag aaccgtgccc agattctgtat caggagccca aatcttctga caaaaactcac 480		
	acatccccac cgccccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540		
	ccaaaaaccca aggacacccct catgatctcc cggacccctg aggtcacatg cgtgggtggtg 600		
	gacgtgagcc acgaagaccc tgaggtcaag ttcaactgtt acgtggacgg cgtggagggtg 660		
	cataatgccca agacaaagcc gcgggaggag cagtacaaca gcacgtaccc tgggtcagc 720		
50	gtcctcaccc tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780		
	aacaaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840		
	gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900		
	ctgacctgcc tggtaaaagg cttctatccc agcgcacatcg ccgtggagtg ggagagcaat 960		
55	ggcagccgg agaacaacta caagaccacg cctccctgtgc tggactccga cgctcccttc 1020		
	ttccctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1080		
	tgcctccgtga tgcataaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1140		
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 <211> 383
 <212> PRT
 <213> Artificial Sequence

10 <220>
 <223> Description of Artificial Sequence: L104EA29LIG
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 1 5 10 15

20 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30

25 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45

30 Tyr Ala Ser Pro Gly Lys Leu Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60

35 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65 70 75 80

40 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
 85 90 95

45 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
 100 105 110

50 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
 115 120 125

55 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
 130 135 140

60 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
 145 150 155 160

65 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
 165 170 175

70 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 180 185 190

75 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 195 200 205

80 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 210 215 220

85 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 225 230 235 240

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 245 250 255
 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
 5 260 265 270
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 275 280 285
 10 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 290 295 300
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 305 310 315 320
 15 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 325 330 335
 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
 20 340 345 350
 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 355 360 365
 25 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 370 375 380
 30 <210> 7
 <211> 1152
 <212> DNA
 <213> Artificial Sequence
 35 <220>
 <223> Description of Artificial Sequence: L104EA29TIG
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 ggcatcgcta gctttgtgtg ttagtatgca tctccaggca aaactactga ggtccgggtg 180
 acagtgcctc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
 gggaatgagt tgacccttc agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaaggtg 360
 45 gagctcatgt acccaccgccc atactacgag ggcataaggca acggaaccca gatttatgta 420
 attgatccag aaccgtgccc agattctgat caggagcccc aatcttctga caaaaactcac 480
 acatccccac cgtccccagc acctgaactc ctggggggat cgtcagttt cctttcccc 540
 cccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtgggtgg 600
 gacgtgagcc acgaaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 660
 50 cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgttaccg tgggtcagc 720
 gtcctcacccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780
 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
 gaaccacagg tgtacaccct gccccatcc cggatgagc tgaccaagaa ccaggtcagc 900
 55 ctgacccgtcc tggtaaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
 gggcagccgg agaacaacta caagaccacg cctccctgtgc tggactccga cgctcccttc 1020
 ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcagggaa cgtcttctca 1080
 tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1140

ccgggttaat ga

1152

5 <210> 8
 <211> 383
 <212> PRT
 <213> Artificial Sequence

10 <220>
 <223> Description of Artificial Sequence: L104EA29TIG
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15 <400> 8
 Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 1 5 10 15

20 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30

25 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45

30 Tyr Ala Ser Pro Gly Lys Thr Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60

35 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65 70 75 80

40 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
 85 90 95

45 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
 100 105 110

50 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
 115 120 125

55 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
 130 135 140

60 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
 145 150 155 160

65 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
 165 170 175

70 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 180 185 190

75 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 195 200 205

80 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 210 215 220

85 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 225 230 235 240

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 245 250 255
 5 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
 260 265 270
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 275 280 285
 10 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 290 295 300
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 15 305 310 315 320
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 325 330 335
 20 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
 340 345 350
 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 25 355 360 365
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 370 375 380
 30 <210> 9
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 35 <220>
 <223> Description of Artificial Sequence: L104EA29WIG
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 ggcacatcgcta gctttgtgt tgagtatgca tctccaggca aatggactga ggtccgggtg 180
 acagtgcctc ggcaggctga cagccaggtg actgaagtct gtgcggcaac ctacatgatg 240
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 50 gacgtgagcc acgaagaccc tgaggtcaag ttcaacttggt acgtggacgg cgtggaggtg 660
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tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagaggct ctccctgtct 1140
ccggtaaat ga 1152

5 <210> 10
<211> 383
<212> PRT
<213> Artificial Sequence

10 <220>
<223> Description of Artificial Sequence: L104EA29WIG
sequence

15 <400> 10
Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1 5 10 15

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
20 25 30

20 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
35 40 45

25 Tyr Ala Ser Pro Gly Lys Trp Thr Glu Val Arg Val Thr Val Leu Arg
50 55 60

30 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65 70 75 80

35 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
85 90 95

40 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100 105 110

45 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
115 120 125

50 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140

55 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
145 150 155 160

60 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
165 170 175

65 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
180 185 190

70 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
195 200 205

75 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
210 215 220

80 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser

	225	230	235	240
	Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys			
	245	250	255	
5	Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile			
	260	265	270	
	Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro			
10	275	280	285	
	Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu			
	290	295	300	
15	Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn			
	305	310	315	320
	Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser			
	325	330	335	
20	Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg			
	340	345	350	
	Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu			
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	ggcatcgcca gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180			
40	acagtgcctc ggcaggctga cagccaggtg actgaagtct gtgcggcaac ctacatgatg 240			
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	gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagg 360			
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	<213> Homo sapiens			
55	<400> 12			
	Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala			
	1	5	10	15

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
20 25 30

5 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
35 40 45

Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
50 55 60

10 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65 70 75 80

Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
15 85 90 95

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100 105 110

20 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
115 120 125

Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140

25 Pro Cys Pro Asp Ser Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser
145 150 155 160

Ser Gly Leu Phe Phe Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser
30 165 170 175

Lys Met Leu Lys Lys Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys
180 185 190

35 Met Pro Pro Thr Glu Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe
195 200 205

Ile Pro Ile Asn
210

40

<210> 13
<211> 1152
<212> DNA
45 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CTLA4Ig
sequence

50

<400> 13
atgggtgtac tgctcacaca gaggacgctg ctcagtctgg tccttgcaact cctgtttcca 60
agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggtaactggc cagcagccga 120
ggcatcgcta gcttgtgtg ttagtatgca tctccaggca aagccactga ggtccgggtg 180
55 acagtgcctc ggcaggctga cagccaggtg actgaagtct gtgcggcaac ctacatgatg 240
ggaaatgagt tgaccttcct agatgattcc atctgcacgg gcacccctcag tggaaatcaa 300
gtgaacctca ctatccaagg actgaggccc atggacacgg gactctacat ctgcaagggtg 360

gagctcatgt acccaccgcc atactacctg ggcataggca acggaaccca gatttatgta 420
attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaaactcac 480
acatccccac cgtccccacg acctgaaactc ctgggtggat cgtcagtctt cctcttcccc 540
ccaaaaccca aggacaccct catgatctcc cggaccctg aggtcacatg cgtgggtgg 600
gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggagg 660
cataatgcca agacaaaagcc gcggggaggag cagtacaaca gcacgtaccg ggtggtcagc 720
gtcctcaccc tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780
aacaaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
gaaccacagg tgtacaccct gccccatcc cggatgagc tgaccaagaa ccaggtcagc 900
ctgacctgcc tggtaaaagg cttctatccc agcgacatcg ccgtggagtggag 960
gggcagccgg agaacaacta caagaccacg cctccgtgc tggactccga cggctccctc 1020
ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtttctca 1080
tgctccgtga tgcattgaggc tctgcacaaac cactacacgc agaagagcct ctccctgtct 1140
ccggtaaat ga 1152

15

<210> 14
<211> 383
<212> PRT
20 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CTLA4Ig
sequence

25

<400> 14
Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1 5 10 15

30

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
20 25 30

35

Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
35 40 45

40

Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
50 55 60

45

Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65 70 75 80

Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
85 90 95

50

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100 105 110

Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
115 120 125

55

Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140

Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
145 150 155 160

Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val

165 170 175

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
180 185 190

5 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
195 200 205

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
10 210 215 220

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
225 230 235 240

15 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
245 250 255

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
20 260 265 270

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
275 280 285

25 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
290 295 300

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
30 305 310 315 320

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
30 325 330 335

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
35 340 345 350

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
35 355 360 365

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
40 370 375 380

<210> 15
<211> 6
45 <212> PRT
<213> Homo sapiens

<400> 15
Met Tyr Pro Pro Pro Tyr
50 1 5

<210> 16
<211> 65
55 <212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer
sequence encoding Oncostatin M-CTLA4 fusion

5 <400> 16
ctcagtctgg tccttgcact cctgtttcca agcatggcga gcatggcaat gcacgtggcc 60
cagcc 65

10 <210> 17
<211> 33
<212> DNA
<213> Artificial Sequence

15 <220>
<223> Description of Artificial Sequence: primer
sequence encoding CTLA4 sequence

<400> 17
20 tttgggctcc tgatcagaat ctgggcacgg ttg 33

25 <210> 18
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer
30 sequence encoding Oncostatin M signal peptide
sequence

<400> 18
35 ctagccactg aagcttcacc aatgggtgta ctgctcacac agaggacgct gctcagtctg 60
gtccttgac tc 72

40 <210> 19
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer
45 sequence from vector sequence

<400> 19
gaggtgataa agcttcacca atgggtgtac tgctcacaca g 41

50 <210> 20
<211> 42
<212> DNA
<213> Artificial Sequence

55 <220>
<223> Description of Artificial Sequence: primer

sequence encoding CTLA4 sequence

<400> 20
gtggtgtatt ggtctagatc aatcagaatc tgggcacggt tc

42

5

DNA SEQUENCING